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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 15:04:29 ; Search time 15.3958 Seconds
(without alignments)
2160.495 Million cell updates/sec

Title: US-09-807-933B-11
Perfect score: 1895
Sequence: 1 MKFSIIASALLLAASSTYAA.....TFKAVTCPAEIIIAKTGCERK 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	672.5	35.5	229	JC7308	cellulase (EC 3.2.1.4)
2	528.5	27.9	511	S10527	endoglucanase B precursor
3	461.5	24.4	393	S59499	cellulase egII - s
4	223	11.8	1832	T31113	mucin-like glycoprotein
5	220.5	11.6	662	A45155	mucin FIM-C.1 - Af
6	208	11.0	327	S20074	promastigote surfa
7	206.5	10.9	371	S20075	larval glue protei
8	202.5	10.7	232	A60095	cellulose 1,4-beta
9	200.5	10.6	471	A26160	cellulose 1,4-beta
10	200.5	10.6	471	A38979	cellulose 1,4-beta
11	199.5	10.5	410	S68153	cellulase (EC 3.2.1.4)
12	192.5	10.2	438	S70602	cellulose 1,4-beta
13	190.5	10.1	770	T22808	hypothetical prote
14	187	9.9	307	GSF23	salivary glue prot
15	187	9.9	866	T45462	membrane glycoprot
16	187	9.9	867	T45463	membrane glycoprot
17	181.5	9.6	217	S01358	salivary glue prot
18	181.5	9.6	263	S01360	salivary glue prot
19	181.5	9.6	795	T20609	hypothetical prote
20	180	9.5	797	VGBEX1	glycoprotein X pre
21	177.5	9.4	418	S28372	cellulase (EC 3.2.1.4)
22	175.5	9.3	851	T22696	hypothetical prote
23	173	9.1	623	T75523	osteoblast specifi
24	170.5	9.0	1235	T13710	protein-tyrosine k
25	167	8.8	339	T25562	hypothetical prote
26	166.5	8.8	856	T00349	Avicelase III - As
27	166	8.8	750	T42614	probable envelope
28	166	8.8	927	T24031	hypothetical prote
29	165	8.7	354	T46740	microfilament shea

30	164.5	8.7	790	2	T34293	hypothetical prote
31	164	8.7	3020	2	A43932	mucin 2 precursor,
32	163.5	8.6	651	2	T21175	hypothetical prote
33	163	8.6	1161	2	S57180	probable membrane
34	162.5	8.6	400	1	A28172	spasmolysin precu
35	162.5	8.6	802	2	A36910	xylanase, beta(1,3
36	162	8.5	796	2	T21460	hypothetical prote
37	161	8.5	389	2	T33340	hypothetical prote
38	161	8.5	708	2	T19474	hypothetical prote
39	160.5	8.5	388	1	JC5461	cellulase (EC 3.2.1.4)
40	158.5	8.4	2225	2	T26063	hypothetical prote
41	158	8.3	645	2	T29818	hypothetical prote
42	157.5	8.3	798	2	T34248	hypothetical prote
43	156.5	8.3	388	1	S43920	cellulase (EC 3.2.1.4)
44	156.5	8.3	693	2	T19551	mucin-like protein
45	154.5	8.2	592	2	T34446	hypothetical prote

ALIGNMENTS

RESULT 1

JC7308
cellulase (EC 3.2.1.4) - Scopulariopsis brevicaulis
N;Alternate names: endoglucanase I
C;Species: Scopulariopsis brevicaulis
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: JC7308; PC7087
R;Nakatani, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.
Bioosci. Biotechnol. Biochem. 64, 1238-1246, 2000
A;Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis
A;Reference number: JC7308
A;Accession: JC7308
A;Molecule type: DNA
A;Residues: 1-229 <NAK>
A;Experimental source: strain TOF-1212
A;Accession: PC7087
A;Molecule type: protein
A;Residues: 21-37;149-164 <NA2>
C;Genetics:
A;Gene: egi
A;Introns: 147/3
C;Keywords: glycosidase; hydrolase

Query Match	35.5%	Score	672.5	DB	2	Length	229
Best Local Similarity	54.0%	Pred. No.	1.8e-39				
Matches	115	Conservative	33	Mismatches	62	Indels	3
Gaps	3						
QY	136	PISGFGNGRTRTRYWDCCKPSCAWDGKASVTK-PVLTC-AKDGVSRLGSDVQSGC-VGG	192				
Db	16	PAASQASCTGTTTRYWDCCKPSCSWDPKAPLSQGPMTCDINDNPLDDGGLTSGCEPGG	75				
QY	193	QAYMCNDNQPWVNDLAVGFAAASLGASAGAFCCGCVLETTTNTAVAGKFFVQVNT	252				
Db	76	GAYMCSHSPWAVDDELAAGAAVNIIGGOTSDWCACYLEFTTGAVSGKQIMVOATNT	135				
QY	253	GGDLSTNHFDLQMPGGVGVGVCQSQWNTTDTGWCARYGGISISECDKLPQLQAGCK	312				
Db	136	GGDLGNHFDIAVMPGGVGVGIFGCTQWGSPPNGWGDYGVVTRADCDSPFPAKAGCE	195				
QY	313	WRFGWFKNADNPVTFKAVTCPAEIIIAKTGCER	345				
Db	196	WRFDWFGGTDNPDVSVREVECPAELVQKSQCQR	228				

RESULT 2

S10527
endoglucanase B precursor - Pseudomonas fluorescens
C;Species: Pseudomonas fluorescens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C;Accession: S10527
R;Gilbert, H.J.; Hall, J.; Hazlewood, G.P.; Ferreira, L.M.A.
Mol. Microbiol. 4, 759-767, 1990

A;Title: The N-terminal region of an endoglucanase from *Pseudomonas fluorescens* subspecies
A;Reference number: S10527; MUID:90355836; PMID:2117693
A;Accession: S10527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-511 <GIL>
A;Cross-references: EMBL:X52615; NID:945497; PIDN:CAA36844.1; PID:945498
C;Superfamily: bacterial cellulose-binding domain homology; glycosidase GWGW domain hom
F;31-128/Domain: bacterial cellulose-binding domain homology <BCB>
F;180-217/Domain: glycosidase GWGW domain homology <GWG>
F;32-127/Disulfide bonds: #status predicted

Query Match 27.9%; Score 528.5; DB 2; Length 511;
Best Local Similarity 31.8%; Pred. No. 3.3e-29;
Matches 122; Conservative 65; Mismatches 136; Indels 61; Gaps 12;

Qy 4 SIASALLAASSTVAECQGYCGGKMTGPTCTGTCVGAENNEWYSQCIP--N 61
Db 136 SSVASS---SSSSVSVSSTRSSSSSVSSVPGTSSSSSSSVLTGAACNWIYGLTFLCN 192

Qy 62 DVOG---NPKTTTTTKAATTKAPVTTTKATTTTKATTTTKAPVTTTKATTTTKTK 117
Db 193 NTSNGWGEDGRCVARTTCSAOPAYGIVSTSSST-----PLSSSSSRSSVASSSSL 246

Qy 118 TTTTKAATTTSSNTGYSPISGFGNGRTRTYWDCKPCSCAMDGKA-SVTKPVLTKAKD 176
Db 247 SSAT---SSSASSSVSPDIDGCG--NGYATRYWDCKPCSCGMSANVPSLVPLQSCSN 301

Qy 177 GVSRLGSDVQSGCGGQAYMCDNDQNPVVNDLALYGFPAASLGSAGASAFCCGCGYELTFT 236
Db 302 NTRLSDVSGSCDGGGYMCWDKIPFAVSPTLAYGAATSSGDV-----CGRCYQLQFT 356

Qy 237 -----NTAVAGKFFVQVNTGDDLTSTNHFDLQMPGGGQVYFNGCOSQWNTND 285
Db 357 GSSYNAPDGPAGALAGKTMTVQATNIGYDVGSGGFDILVEGGVGAFNACSAQWYSNA 416

Qy 286 GHWARYGGI-----SSISE-----CDKL-----PQLQAGCKRFGWFKNA 321
Db 417 ELGATGGFLACKQOLGYNASLSQYKSVLNRCDSPVSGRLTQLQOQCTWFAEWFEAA 476

Qy 322 DNPVTFKAVTCAPIIAKTGCR 345
Db 477 DNFLKLYKEVPCPAELTTRSGMNR 500

RESULT 3
S59499
C;Species: *Ustilago maydis* (corn smut)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
C;Accession: S59499
R;Schaecker, F.; Wanner, G.; Kahmann, R.
Biol. Chem. Hoppe-Seyler 376, 617-625, 1995
A;Title: Filament-specific expression of a cellulase gene in the dimorphic fungus *Ustilago maydis*
A;Reference number: S59499; MUID:96145728; PMID:8590631
A;Accession: S59499
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-393 <SCH>
A;Cross-references: GB:S81598; NID:g1478378; PIDN:AAB36147.1; PID:g1478379

Query Match 24.4%; Score 461.5; DB 2; Length 393;
Best Local Similarity 44.7%; Pred. No. 1.1e-24;
Matches 97; Conservative 27; Mismatches 72; Indels 21; Gaps 9;

Qy 145 GRTRYWDCKPCSCAMDGKASVTKPVLTKADGVSRLGS----DVQSGCGVGOAYMCDND 200
Db 27 GMATRYWDCKLASASWEGKAPVAPVDACKADGVTLLDSKKDPGSGCGNGKNCMSQW 86

Qy 201 QPWWVND--LAYGFAASLGSAGASAFCCGCGYELTFTNTAVAGK-----KFVVQVNTNG 253
Db 87 QPDEDTPTLAFGFGAFTTQ--ESDTCACFAEFEDA-QGKAMKRNKLIQVQVNTNG 143

254 DDLSTNHFDLQMPGGGQVYF-NCCQSQWNTNTDQWARYGGISSISSECDKLPQLQAGCK 312
Db 144 GDVQSQNFQIFGGGLGAPKGPQWQVGLGQVGVKSAATECSKLPKPLQEGCK 203

Qy 313 WRFG-WFNADNPEV--TFKAVTCAPIIAKTGCRK 346
Db 204 WRFSEW---GDNVPLKSGPKRVRKPSKSLIDRSGCQRK 237

RESULT 4
T31113
mucin-like glycoprotein 900 - *Cryptosporidium parvum*
C;Species: *Cryptosporidium parvum*
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31113
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Goussset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubre
Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of *Cryptosporidium parvum* mediate
A;Reference number: Z20989; MUID:99066935; PMID:9851610
A;Accession: T31113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1832 <BAR>
A;Cross-references: EMBL:AF068065; NID:g4063041; PID:g4063042; PIDN:AAC98153.1

Query Match 11.8%; Score 223; DB 2; Length 1832;
Best Local Similarity 31.1%; Pred. No. 1.3e-07;
Matches 83; Conservative 21; Mismatches 109; Indels 54; Gaps 9;

Qy 68 PXTTTTTTKAATTKAPVTTTKATTTTKAPVTTTKATTTTKATTTTKATTTTKATTTT 127
Db 419 PTT 478

Qy 128 SSSNTGYSPISGFGNGRTRTYWDCKPCSCAMDGKA-----SVTKPVLTC--AKDG 177
Db 479 TTTTTTATTTTKPTT 538

Qy 178 VSRLGSDVSGCGV-----GOAYMCDNDQNPVVND--LAYGFAASLGS----- 221
Db 539 ECEAKGATVVGIVGDKDRIENGAF-----TWIPNDTHVRFKVDVGNVTISVRCKG 592

Qy 222 GASAFCCGCGYELTFTNTAVAGK---KFVVQVNTG-----DDLSTNHFDLQMPGGG 269
Db 593 GAGKLEFPDRSLDFTIPPVAGHNSCSIIVGVSGGKIHVSYPYSGKDVSLISAPIQ----- 647

Qy 270 VGFNGCQSQWNTNTDQWARYGGISS 296
Db 648 -----PCELFNEVYCDTCTAKYGAHNS 669

RESULT 5
A45155
mucin FIM-C.1 - African clawed frog (fragment)
C;Species: *Xenopus laevis* (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C;Accession: A45155
R;Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C)
A;Reference number: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
A;Cross-references: GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
C;Superfamily: trefoil homology
F;162-202/Domain: trefoil homology <TRF1>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>

Query Match	10.6%;	Score 200.5;	DB 1;	Length 471;
Best Local Similarity	32.4%;	Pred. No. 1.2e-06;		
Matches 48;	Conservative	26;	Mismatches 41;	Indels 33;
				Gaps 6;

[illegible]

RESULT 11

S58153
cellulase (EC 3.2.1.4) 3D precursor - Penicillium janthinellum
N:Alternate names: 3D endoglucanase 2; endo-1,4-beta-glucanase
C:Species: Penicillium janthinellum
C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 18-Jun-1999
C:Accession: S58153; S57950
R:Mernitz, G.; Koch, A.; Henrissat, B.; Schulz, G.
Curr. Genet. 29, 490-495, 1996
A:Title: Endoglucanase II (EGII) of Penicillium janthinellum: cDNA sequence, h
A:Reference number: S58153; MUID:96207475; PMID:8625430
A:Accession: S58153
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-410 <MR>
A:Cross-references: EMBL:X89564; NID:G984165; PIDN:CAA61740.1; PID:G984166
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1
C:Function:
C:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans
A:Pathway: cellulose degradation
C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homo
C:Keywords: glycosidase; hyaluron; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-410/Product: cellulase #status predicted <MAT>
F;22-410/Product: cellulase #status predicted <MAT>
F;22-410/Product: cellulase #status predicted <MAT>

Query Match	10.5%;	Score 199.5;	DB 1;	Length 410;
Best Local Similarity	23.9%;	Pred. No. 1.3e-06;		
Matches	80;	Conservative 43;	Mismatches 113;	Indels 99;
				Gaps 12;

9	ALLAAS	TY	AAEC	SQ	YG	CG	CK	MM	WT	GP	TC	SG	FT	CG	AA	NN	EY	SQ	IC	PN	DV	Q	GN	P	6
11	ALLALG	Db	SALG	Q	Q	T	A	---	WG	CG	GG	WT	G	AT	CV	S	Y	Y	C	---	SF	Q	N	N	59
12	KT	TY	TTTT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	128	
19	SS	TY	NTG	Y	P	I	S	---	GF	SG	NR	TR	TY	WD	CK	P	S	C	A	W	D	G	K	18	
20	SAP	Db	T	K	V	R	F	A	G	N	I	A	G	T	A	G	T	A	G	T	A	G	T	A	13
185	V	Q	S	C	V	G	G	Q	A	Y	M	C	N	D	N	P	W	V	N	D	D	L	A	Y	24
134	V	Q	N	A	D	T	F	---	N	I	F	R	L	T	G	W	Q	F	I	V	N	N	L	18	
245	F	Q	V	Q	N	T	G	D	L	S	T	N	H	D	L	O	M	P	G	G	V	G	Y	F	30
182	C	Q	I	V	I	D	H	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	21	
305	T	Q	O	L	A	G	K	W	R	F	G	W	F	K	N	A	D	N	P	E	V	T	F	K	319
216	T	Q	A	V	E	N	S	V	T	I	G	I	N	N	E	P	H	D	I	N	I	A	T	A	250

RESULT 12

```

116 RTTTTPTTTTTRTTTPTTTTTRTTTPTTTTTRTTTPTTTTTRTTTPTTTTTRPTT 175
138 SGGSGNGRITTRYWDCKPSCAWDGKASVTKPVLTKAKDG 177
176 P-----TFTO-----KPMCPMKPCGGPGKPCVGCPRRG 202

```

RESULT 9
A26160
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei)
N:Alternate names: exo-cellobiohydrolase II
C:Species: Trichoderma reesei
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26160; A26472
R:Chen, C.M.; Gritzali, M.; Stafford, D.W.
Bio/Technology 5, 274-278, 1987
A:Title: Nucleotide sequence and deduced primary structure of cellobiohydrolase II from
A:Reference number: A26160

A;Residues: 1-471 <CHE>
R;Teeri, T.T.; Lehtovaara, P.; Kauppinen, S.; Salovuori, I.; Knowles, J.
Gene 51, 43-52, 1987
A;Title: Homologous domains in Trichoderma reesei cellulolytic enzymes: gene sequence analysis
A;Reference number: A26472; MUID:87248061; PMID:3596237
A;Accession: A26472
A;Molecule type: DNA
A;Residues: 1-471 <TEE>
A;Cross-references: GB:M16190; NID:gl70540; PIDN:AAA34210.1; PID:gl70541
C;Genetics:
C;Introns: 31/2; 160/2; 243/1
C;Superfamily: cellulose 1,4-beta-cellobiosidase II; fungal cellulose-binding domain homolog
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: cellulose-binding domain homology <FCB>

Query Match	10.6%	Score 200.5;	DB 1;	Length 471;
Best Local Similarity	32.4%	Pred. No. 1.2e-06;		
Indels	33;	Mismatches 41;	Caps 6;	

[illegible]

QY
116 TKTTTTKAAATTTSSN--TGYSPIGGF 141

RESULT 10
A38979
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride)
Cispecies: trichoderma viride revision 10-Sep-1999 #text change 10-Sep-1999

C/Accession: A38979
C/Author: Wang, J.R.; Zhang, M.F.; Huang, T.
C/Genet. Sin. 22, 74-80, 1995
C/Title: The primary structure of cellobiohydrazase gene (CBH II) from *Trichoderma viride*.
C/Reference number: A38979
C/Accession: A38979
C/Molecule type: DNA
C/Residues: 1-471 <WAN>
C/Genetics:
C/Gene: cbhII
C/Introns: 31/2; 160/2; 243/1
C/Superfamily: cellulase 1,4-beta-cellobiosidase II; fungal cellulose-binding domain how
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
C/Domain: 31-62/Domain: fungal cellulose-binding domain homology <FCB>

S70602
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - cultivated mushroom
N:Alternate names: cellulase
C:Species: Agaricus bisporus (cultivated mushroom)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S70602
R:Yaguchi, E.; Chow, C.M.; Challen, M.P.; Thurston, C.P.
Curr. Genet. 30, 56-61, 1996
A:Title: Correlation of exons with functional domains and folding regions in a cellulase
A:Reference number: S70602; MUID:96269930; PMID:8662210
A:Accession: S70602
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <YAG>
A:CROSS-references: EMBL:Z34007; NID:g1494969; PIDN:CAA83971.1; PID:g1494970
C:Genetics:
A:Introns: 34/1; 56/2; 96/3; 202/1; 325/3; 410/2
C:Superfamily: cellulose 1,4-beta-cellobiosidase II; fungal cellulose-binding domain hom
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:25-56/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 10.2%; Score 192.5; DB 1; Length 438;
Best Local Similarity 29.9%; Pred. No. 4.1e-06;
Matches 61; Conservative 26; Mismatches 84; Indels 33; Gaps 8;

QY 9 ALLLAASST---YAAECGQYGGGKMTGPTCTCTSGFTCVGAENNEWYSQCIPNDQVQ 65
DB 5 AALLALASLVPGFVQAGSPWVGCGGNGWTGPTTCASGTCV--KQNDFFYSQCLPNNQA- 61

QY 66 GNPKTITTTT---TTKAAATTKAPVTTTKA-----TTTTTKAP-----VTTTKATTTTTHK 113
DB 62 --PPSTTGTGTPPTATTTTSGGTSGAGNPTGKTVLWSPFYADEVAQAADISNPISL 119

QY 114 TTTTKTTTAAATTTSSNTGYSPIGSGFGNGRTTRW-----DCKPSCAWDG 162
DB 120 ATKAASVAKIPTFVWFDTVAKVPLDGLGYLADRSKNQLVQIVVYDLPDRDCA--ALASNG 177

QY 163 KASVTKPVLTCADGVSRLGSDVQ 186
DB 178 EFLSLANDGLNKYKYNVDQIAAQIK 201

RESULT 13
T22808
hypothetical protein F56H9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22808
R:Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19618
A:Accession: T22808
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-770 <WIL>
A:CROSS-references: EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F56H9.1
A:Experimental source: clone F56H9
C:Genetics:
A:Gene: CESP:F56H9.1
A:Map position: 5
A:Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Query Match 10.1%; Score 190.5; DB 2; Length 770;
Best Local Similarity 33.5%; Pred. No. 9.7e-06;
Matches 61; Conservative 12; Mismatches 54; Indels 55; Gaps 9;

QY 30 GGNK---WTGPTC--CTSGFTCVGAENNEWYS-----QCIPNDQVQNP 68
DB 503 GGKLVTVKTLTIFRFLSNFKCV---MKWISTLLHLLTYKLDVINSIATSP-ADP 557

QY 69 KTTT-----TTTKAATTKAPV-----TTTKATTTTTHKAPVTTTKAT----- 107
DB 558 TTTTTEATTTTTEITTTTTEVTTTTPVTTTTTTTSTTTTSTTTTPTTTTTTTTTTTTTS 617

QY 108 TTTTTKTTTTHKATTTSSNTGYSPIGSGFGNGRTTRWDCKPSCAWDGKASVT 167
DB 618 TTTTSTTTTPTTTTSTTTTSTTTTATPTT-----TTTTMPFCNPVNSLGMGDAN 669

QY 168 KP 169
DB 670 NP 671

RESULT 14
GSFF3
salivary glue protein sgs-3 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 16-Jul-1999
C:Accession: A03329
R:Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
J. Mol. Biol. 168, 765-789, 1983
A:Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila
A:Reference number: A92904; MUID:83294545; PMID:6411930
A:Accession: A03329
A:Molecule type: DNA
A:Residues: 1-307 <CAR>
A:CROSS-references: GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989
C:Comment: This protein is produced by third-instar larvae.
C:Genetics:
A:Gene: sgs-3
A:CROSS-references: FlyBase:FBgn0003373
A:Map position: 3L (68C)
A:Introns: 10/1
C:Superfamily: salivary glue protein
C:Keywords: salivary gland; tandem repeat

Query Match 9.9%; Score 187; DB 1; Length 307;
Best Local Similarity 35.5%; Pred. No. 6.9e-06;
Matches 66; Conservative 17; Mismatches 59; Indels 44; Gaps 11;

QY 1 MKFSI---IASALLAASSTYAAECGQYGGGKMTGPTCTCTSGFTCVGAENNEWYSQ 57
DB 1 MKLTATATLASILLIGSAN--VANCC-----DCG-----CPTTTTTC- 36

QY 58 CIPNDQVQGNPKTTTTTTTKAA-----TTTKAPVTTTKATTTT---TTTKAPVTTTKATTTT 110
DB 37 --PRTTQPPCTTTTTTTTTTTCAPPTQOSTTQPPCTTSKPTTKQTTLQPLCTTTPTTKAT 94

QY 111 TTK-TTTTKTTTKAAT---TTSSNTGYSPIGSGFGNGRTTRWDCKPSCAWDGKASV 166
DB 95 TTKPTTTTKATTTTKATTTTKQTTLQPLCTTP-TTTKQTTLQPLCTTPTTT---KPTT 150

QY 167 TKPVL 172
DB 151 TKPTT 156

RESULT 15
T45462
membrane glycoprotein [imported] - equine herpesvirus 1
C:Species: equine herpesvirus 1
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000
C:Accession: T45462
R:Kirisawa, R.; Kobayashi, T.; Kawakami, Y.; Iwai, H.
J. Equine Sci. 7, 79-87, 1996
A:Title: Nucleotide sequences of open reading frames 1, 24 and 71 of an attenuated equine
A:Reference number: Z22973
A:Accession: T45462
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-866 <KIR>
A:CROSS-references: EMBL:D88733; PIDN:BAA20037.1
A:Experimental source: strain HH1
C:Genetics:
A:Note: ORF71
C:Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein hom

us-09-807-933b-11.rpr

Wed Jun 18 17:55:06 2003

F;558-866/Domain: equine herpesvirus 1 glycoprotein homology <EHG>

Query Match 9.9%; Score 187; DB 2; Length 866;
 Best Local Similarity 48.6%; Pred. No. 1.9e-05;
 Matches 52; Conservative 7; Mismatches 38; Indels 10; Gaps 4;
 Qy 70 TTTTITTKAATTKAPVTTTKATTTTITTKAPVTTTKATTT--TTTITTKTTTITTKAATTT 127
 Db 267 TTTAATTTAATTTAA--TTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 324
 Qy 128 SSSNTGYSPISGPGSGNGRTTRWDCKPSCANDGKASVTKPVLTC 174
 Db 325 AATTG-SPTSGSTSTTGAST-----STPSASTATGATPTSTSTSA 365

Search completed: June 18, 2003, 17:16:21
 Job time : 17.3958 secs